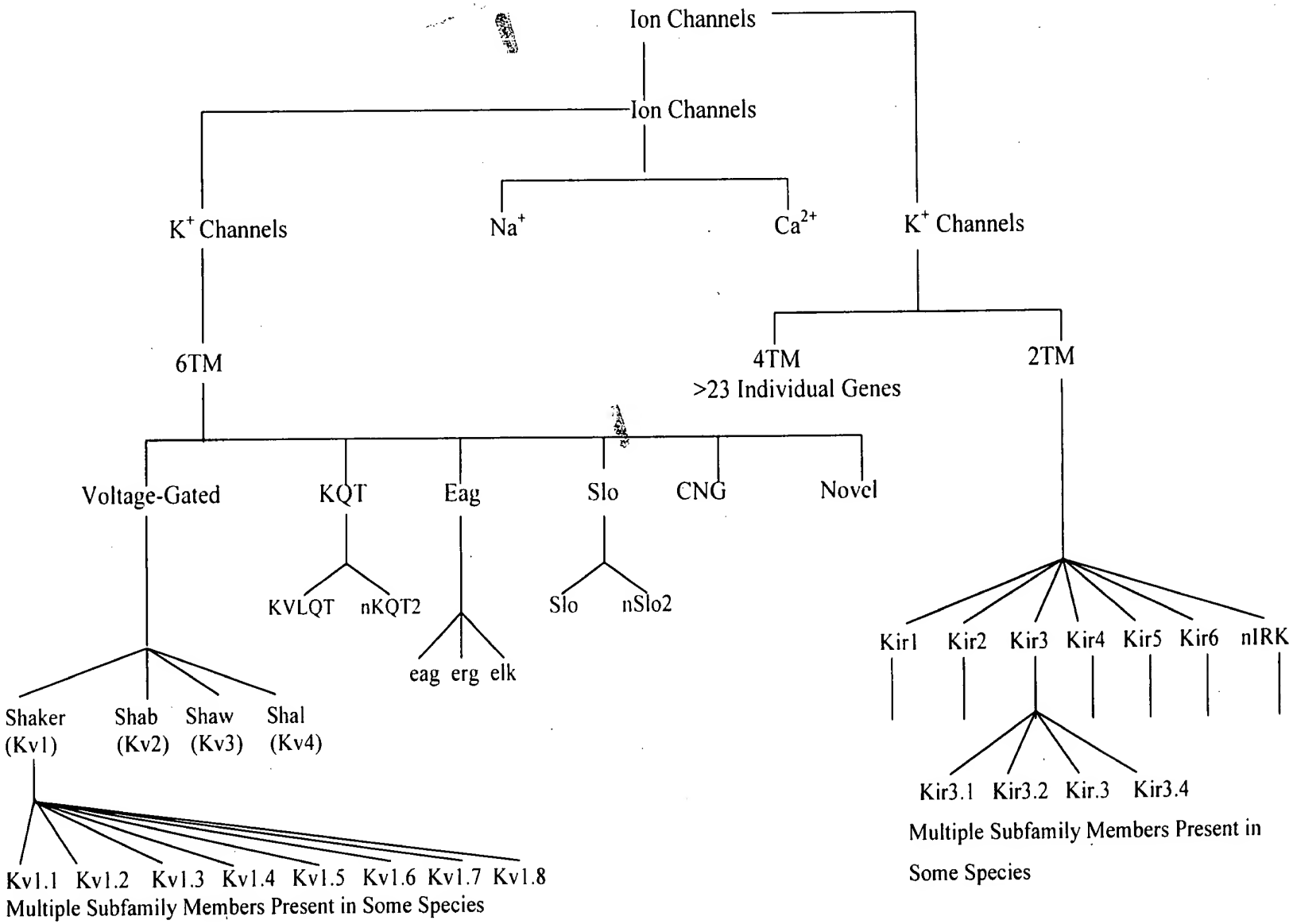

Fig. 1

417177_1

09/786108

DOCKET NO: 0887-4138PC1

Fig. 2

```
elk1  ---MPVMKGLLAPQNTFLDTIATRFDGTHSNFILANAQVAKGFPIVYCSD  47
erg1  ---MPVRRGHVAPQNTFLDTIIRKFEGQSRKFIIANARVEN-CAVIYCND  46
eag1  MTMAGGRRGLVAPQNTFLENIVRRS--NDTNFVLGNAQIVD-WPIVYSND  47

elk1  GFCELAGFARTEVMQKSCSCKFLFGVETNEQLMLQIEKSLEEKVEFKGEI  97
erg1  GFCELCGYSRAEVMQRPCTCDFLHGPRTQRRAAAQIAQALLGAEERKVEI  96
eag1  GFCKLSGYHRAEVMQKSSACSFMYGELTDKDTVEKVRQTFENYEMNSFEI  97

elk1  MFYKKNGAPFWCLLDIVPIKNEKGDVVLFLASFKDITDTKVKITSEDKKE  147
erg1  AFYRKDGSCFLCLVDVVPVKNEDGAVIMFILNFEVVMEKDMVGSPAHDTN  146
eag1  LMYKKNRTPVWFFVKIAPIRNEQDKVVLFLCTFSDITA--FK-QPIKDDS  144

elk1  DRAK----------------------GRSR-------------------A  156
erg1  HRGPSTSWLASGRAKTFRLKLPALLALTARESPMRTGSTGSPGAPGAVVV  196
eag1  CKG----------------------WGKFAR-------------------  153

elk1  GSHFDSARRRS----------R----------------------------  168
erg1  DVDLTPAAPSSESLALDEVSAMDNHVAGLGPAEERRALVGPASASPVASI  246
eag1  ---LTRALTSS----------R-------G--------------------  163

elk1  ------AVLYHISGHLQ-----------------------------------  179
erg1  PGPHPSPRAQSLNPDASGSSCSLARTRSRESCASVRRASSADDIEAMRAG  296
eag1  -------VLQQLAPSVQ-----------------------------------  173

elk1  ----------------------------------------------------  179
erg1  ALPLPPRHASTGAMHPLRSGLLNSTSDSDLVRYRTISKIPQITLNFVDLK  346
eag1  ----------------------------------------------------K  174

elk1  ------------------RREKNK---LKINNNVFVDKPAFPEYKVSDAK  208
erg1  GDPFLASPTSDREIIAPKIKERTHNVTEKVTQVLSLGADVLPEYKLQAPR  396
eag1  G-----------------ENVHKH---SRLAEVLQLGSDILPQYKQEAPK  204

                    ----------S1----------
elk1  KSKFILLHFSTFKAGWDWLILLATFYVAVTVPYNVCFIGNED--LS----  252
erg1  IHRWTILHYSPFKAVWDWLILLLVIYTAVFTPYSAAFLLKETEDGSQAPD  446
eag1  PPHIILHYCVFKTTTWDWIILILTFYTAILVPYNVSFKTRQN-N------  247

                ----------S2----------              --
elk1  ---TTRSTTVSDIAVEILFIIDIILNFRTTYVSKSGQVIFEARSICIHYV  299
erg1  CGYACQPLAVVDLLVDIMFIVDILINFRTTYVNANEEVVSHPGRIAVHYF  496
eag1  -----VAWLVVDSIVDVIFLVDIVLNFHTTFVGPAGEVISDPKLIRMNYL  292
```

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Fig. 2 (Cont'd)

```
       ------S3---------                  ------------S4-------
elk1   TTWFIIDLIAALPFDLLYAFNVTVVS---LVHLLKTVRLLRLLRLLQKLD  346
erg1   KGWFLIDMVAAIPFDLLIFGSGSEE----LIGLLKTARLLRLVRVARKLD  542
eag1   KTWFVIDLLSCLPYDVINAFENVDEGISSLFSSLKVVRLLRLGRVARKLD  342

       -       ---------S5----------
elk1   RYSQHSTIVLTLLMSMFALLAHWMACIWYVIGKMEREDNSLLKWEVG-WL  395
erg1   RYSEYGAAVLFLLMCTFALIAHWLACIWYAIGNMEQPHMDSHIG----WL  588
eag1   HYIEYGAAVLVLLVCVFGLAAHWMACIWYSIGDYEIFDEDTKTIRNNSWL  392

                  --------------------P--------------------
elk1   HELGKRLESPYYGNN-----TLGGPSIRSAYIAALYFTLSSLTSVGFGNV  440
erg1   HNLGDQIGKPYNSSG------LGGPSIKDKYVTALYFTFSSLTSVGFGNV  632
eag1   YQLALDIGTPYQFNGSGSGKWEGGPSKNSVYISSLYFTMTSLTSVGFGNI  442

              ----------S6-------------
elk1   SANTDAEKIFSICTMLIGALMHALVFGNVTAIIQRMYSRWSLYHTRTKDL  490
erg1   SPNTNSEKIFSICVMLIGSLMYASIFGNVSAIIQRLYSGTARYHTQMLRV  682
eag1   APSTDIEKIFAVAIMMIGSLLYATIFGNVTTIFQQMYANTNRYHEMLNSV  492

elk1   KDFIRVHHLPQQLKQRMLEYFQTTWSVNNGIDSNELLKDFPDELRSDITM  540
erg1   REFIRFHQIPNPLRQRLEEYFQHAWSYTNGIDMNAVLKGFPECLQADICL  732
eag1   RDFLKLYQVPKGLSERVMDYIVSTWSMSRGIDTKKVLQICPKDNRADICV  542

                                          ------------------
elk1   HLNKEILQLS-LFECASRGCLRSLSLHIKTSFCAPGEYLLRQGDALQAIY  589
erg1   HLNRSLLQHCKPFRGATKGCLRALAMKFKTTHAPPGDTLVHAGDLLTALY  782
eag1   HLNRKVFKEHPAFRLASDGCLRALAMEFQTVHCAPGDLIYHAGEDVDSLC  592

       ----------cNBD-------------------------------------
elk1   FVCSGSMEVLKDSMVLAILGKGDLIGANLSIKDQVIKTNADVKALTYCDL  639
erg1   FISRGSIEILRGDVVVAILGKNDIFGEPLNLYARPGKSNGDVRALTYCDL  832
eag1   FVVSGSLEVIQDDEVVAILGKGDVFGDVFWKEATLAQSCANVRALTYCDL  642

elk1   QCIILKGLFEVLGLYPEYAHKFVEDIQHDLTYNLREGHESDVISRLSNKS  689
erg1   HKIHRDDLLEVLDMYPEFSDHFWS--SLEITFNLRDTNMIPG--------  872
eag1   HVIKRDALQKVLEFYTAFSHSFSR--NLILTYNLRKRIVFR---------  681

elk1   TVPQAEPKGNGSIKKRLPSIVEDEEEEEVEEEETTSLSPIYTRGSSVSHS  739
erg1   ----------------SPSSAELESGFNRQ------------RKRKLSFR  894
eag1   ----------------KISDVKREEEERMK------------RKNEAPLI  703
```

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Fig. 2 (Cont'd)

```
elk1  KKTGSSKSYLGLSLKQLTSGTVPFHSPIRVSSANSPKTKQEADPPNHGTR  789
erg1  RRTDKDTEQPGEVSALG-------QGPARVGPGPSCRG-QPGGPWGESP-  935
eag1  LPPDHPVRRLFQRFRQ--------QKEARLAAE---RGGRDLDDLDVEK-  741

elk1  KEKNLKVQLCSLGTAGTPELSPRIVDGIEDGNSSEETQTFDFGSEQIRPE  839
erg1  ------------SSGPSSPES-----------SEDEGPGRSSSPLRLVPF  962
eag1  ------------GNALTDHTS-----------ANHSLVKASVVTVRESPA  768

elk1  PRISPSLGESEIGAAFLFIKAEETKQQINKLNSEVTTLTQEVSQLGKDMR  889
erg1  S--SPRPPGDSPGGEPLTEDGEKSSDTCNPLSGAFSGVSN-IFSFWGDSR  1009
eag1  TPVSFQAASTSTVSDHAKLHAP-GSECLGPKAGGGDPAKRKGWARFKDAC  817

elk1  SI-MQLLENILSPQQPSQFCSLHPTSICPSRESFQTRVSWSAHQPCLHLQ  938
erg1  GRQYQELPRCPAP--------------APSLLNIPLSSPG------RRSR  1039
eag1  GK--GEDWNKVSK--------------AESMETLPERTKASGEATLKKTD  851

elk1  ANGAHLYHGNVTSDIWSVDPSLVGSNPQRTEAHEQSPVDSELHHSPNLAY  988
erg1  GD---------VESRLDALQRQDNRLETRLSAD-MATVLQLLQRQMTLVP  1079
eag1  SC---------DSGITKSDLRLDNVGEAPSPQD-RSPILAEVKHSFYPIP  891

elk1  SPSHCQVIQEGHLQFLRCISPHSDTTLTPLQSISATLSSSVCSSSETSLH  1038
erg1  PAYSAVTTPG-----------PGPTSTSPLLPVGPVPTLTLDSLSQVSQF  1118
eag1  EQTLQATVLE-----------VKHELKEDIKALNAKMTSIEKQLSEILRI  930

elk1  LVLPSRSEEGSITHGPVSSFSLENLPGSWDREGMMSASTEPLENFPVEVV  1088
erg1  VAFEEL-PAGAPELPQDGPTRRLSLPGQLG-----ALTSQPLHRHGSDPG  1162
eag1  LMSR-----GSSQSPQD--ICEVSRP--Q---------S-PESDRDIFGA  961

elk1  TSTADVKDSKAINV  1102
erg1  S-------------  1163
eag1  S-------------  962
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Key: *elk1* (SEQ ID NO:2)
erg1 (SEQ ID NO:15)
eag1 (SEQ ID NO:16)

Fig 3

```
CGGGATCCTT GTGGACAAAC TTTGATGGGG AATTTCACAC      40
AGCGCTGGAA AAATGCCGGT TATGAAAGGA TTGCTGGCGC      80
CACAGAACAC CTTCCTGGAC ACTATTGCCA CCCGTTTCGA     120
CGGAACACAT AGCAACTTCA TCCTGGCCAA TGCCCAAGTG     160
GCAAAAGGTT TCCCCATAGT CTACTGTTCA GATGGCTTCT     200
GTGAGCTGGC TGGGTTTGCT CGAACTGAAG TCATGCAGAA     240
GAGTTGCAGC TGCAAGTTTC TGTTTGGGGT GGAGACCAAC     280
GAGCAGCTGA TGCTTCAGAT CGAAAAGTCC CTGGAGGAGA     320
AGGTAGAGTT CAAAGGAGAA ATTATGTTCT ACAAGAAGAA     360
TGGGGCTCCA TTTTGGTGCC TGTTGGATAT CGTTCCTATA     400
AAGAATGAGA AAGGAGATGT GGTCCTTTTC CTGGCCTCAT     440
TCAAAGATAT AACAGACACG AAAGTGAAGA TTACTTCAGA     480
AGATAAAAAA GAAGACAGAG CCAAAGGAAG ATCAAGAGCA     520
GGGAGCCACT TCGACTCAGC CCGCAGACGG AGCCGAGCAG     560
TCCTTTATCA CATCTCAGGA CACCTGCAAA GAAGAGAAAA     600
GAACAAATTG AAAATAAATA ATAACGTGTT TGTAGATAAA     640
CCGGCGTTTC CAGAGTATAA GGTTTCCGAT GCAAAAAAGT     680
CCAAGTTCAT CCTGCTGCAC TTCAGCACTT TTAAAGCTGG     720
CTGGGACTGG CTCATTTTGC TGGCAACGTT TTATGTTGCT     760
GTGACAGTCC CTTACAACGT GTGCTTCATT GGCAATGAGG     800
ATCTGTCCAC AACTCGGAGC ACAACGGTCA GTGACATCGC     840
TGTGGAGATT CTCTTCATTA TAGATATTAT TCTAAATTTC     880
CGAACAACTT ATGTCAGCAA GTCTGGCCAA GTTATCTTTG     920
AAGCGAGATC CATTTGCATC CACTACGTCA CCACCTGGTT     960
CATCATTGAT CTGATTGCTG CCCTGCCCTT TGACCTCCTG    1000
TATGCTTTCA ATGTCACAGT GGTGTCCCTC GTACATCTTC    1040
TGAAGACTGT TCGGCTGCTC CGTCTTTTGC GCCTCCTGCA    1080
GAAGCTGGAC CGTTATTCTC AGCACAGCAC AATTGTCCTC    1120
ACCCTGCTCA TGTCCATGTT TGCTCTCCTT GCACACTGGA    1160
TGGCATGTAT CTGGTATGTC ATTGGAAAAA TGGAGAGGGA    1200
GGACAACAGC CTTCTCAAGT GGGAAGTCGG TTGGCTTCAC    1240
GAGCTGGGAA AGAGACTGGA ATCTCCGTAC TACGGCAACA    1280
```

Fig. 3 (Cont'd)

ACACGCTGGG CGGCCCGTCC ATCCGCAGTG CCTATATCGC 1320
AGCCTTGTAC TTCACTCTCA GCAGCCTCAC CAGCGTGGGA 1360
TTTGGGAATG TGTCCGCTAA CACGGATGCA GAGAAGATCT 1400
TCTCCATCTG TACCATGTTG ATTGGAGCCC TGATGCATGC 1440
CTTGGTATTT GGGAATGTGA CTGCCATCAT ACAGAGAATG 1480
TACTCTAGAT GGAGCCTGTA CCATACTAGA ACCAAGGACC 1520
TAAAGGACTT CATCCGTGTG CATCACCTGC CCCAGCAACT 1560
CAAGCAGAGG ATGCTTGAGT ACTTTCAGAC AACTTGGTCT 1600
GTCAACAATG GAATAGATTC AAATGAGCTT TTGAAAGACT 1640
TTCCAGATGA GCTGCGCTCT GACATCACAA TGCATCTGAA 1680
CAAGGAGATC TTACAGCTGT CCCTGTTTGA ATGTGCTAGC 1720
CGGGGCTGCC TCAGGTCTCT GTCTCTCCAT ATTAAAACCT 1760
CATTCTGTGC CCCAGGAGAG TATCTGCTGC GCCAGGGAGA 1800
TGCGTTGCAG GCCATCTACT TCGTGTGCTC AGGCTCTATG 1840
GAGGTTCTTA AAGACAGCAT GGTGTTGGCT ATTCTAGGGA 1880
AGGGGGATTT AATTGGAGCA AATTTATCAA TTAAAGACCA 1920
AGTGATCAAG ACCAACGCTG ACGTGAAGGC TCTGACCTAC 1960
TGTGATCTAC AGTGCATCAT CCTGAAAGGT CTCTTTGAGG 2000
TGCTGGGCCT TTACCCAGAG TACGCACACA AATTCGTAGA 2040
AGACATCCGC ACGACCTCAC ATACAACCTT CGAGAAGGTC 2080
ATGAGAGTGA TGTAATATCA AGATTATCGA ACAAATCTAC 2120
AGTCCCACAG GCAGAGCCCA AGGGGAATGG AAGCATCAAG 2160
AAGAGACTCC CATCCATTGT GGAAGATGAG GAAGAGGAGG 2200
AAGTGGAGGA AGAGGAGACC ACCTCCCTTT CTCCCATCTA 2240
CACAAGGGGA TCCTCTGTTT CACACAGCAA AAAGACTGGA 2280
AGCAGTAAGA GCTATCTAGG TTTGAGCTTA AAGCAACTGA 2320
CCTCAGGAAC AGTTCCATTC CACTCACCTA TCAGAGTCTC 2360
CAGTGCCAAC TCCCCTAAAA CCAAGCAGGA AGCTGACCCA 2400
CCTAACCATG GCACACGGAA AGAGAAGAAT CTGAAAGTTC 2440
AGCTCTGCAG CCTGGGTACT GCTGGAACCC CAGAGCTCAG 2480
TCCGAGGATT GTCGATGGAA TTGAAGATGG CAACAGCAGT 2520
GAGGAAACTC AGACTTTTGA TTTTGGCTCT GAACAAATCA 2560

Fig. 3 (Cont'd)

GGCCAGAGCC CAGGATTTCC CCTTCCCTTG GAGAATCAGA 2600
GATTGGAGCT GCGTTTCTGT TCATCAAGGC TGAAGAAACC 2640
AAGCAGCAGA TAAACAAGCT CAACAGTGAG GTCACAACAT 2680
TGACTCAGGA GGTCTCCCAG CTAGGGAAAG ATATGAGAAG 2720
CATCATGCAA CTTCTGGAAA ACATCTTGTC ACCTCAGCAG 2760
CCATCACAAT TTTGTTCTCT GCATCCCACT TCAATCTGTC 2800
CTTCCAGAGA AAGTTTCCAG ACTAGGGTGA GCTGGAGTGC 2840
TCACCAGCCT TGCCTACACT TGCAGGCAAA TGGAGCACAT 2880
CTTTACCATG GCAATGTCAC CTCTGACATC TGGAGTGTCG 2920
ACCCCTCCTT GGTGGGCAGC AACCCTCAAC GAACTGAAGC 2960
TCATGAGCAA AGTCCAGTAG ATAGTGAACT GCATCATTCT 3000
CCAAACCTGG CTTATTCCCC CTCTCACTGC CAGGTTATCC 3040
AAGAAGGCCA CTTGCAGTTC CTAAGGTGCA TCTCCCCTCA 3080
TTCAGATACC ACACTGACAC CTTTGCAGTC CATCTCAGCC 3120
ACTCTCTCAT CCTCTGTGTG CTCCTCATCA GAAACATCCT 3160
TGCACCTCGT TCTCCCAAGT AGGTCAGAGG AGGGCAGCAT 3200
CACTCATGGA CCTGTGAGTT CTTTCAGTTT GGAAAACTTA 3240
CCAGGATCTT GGGACCGAGA AGGAATGATG TCAGCCTCTA 3280
CAGAACCCTT GGAGAACTTT CCAGTAGAAG TTGTCACAAG 3320
CACAGCGGAT GTAAAAGACA GCAAAGCCAT AAACGTATAA 3360
TATCAGCACA TAAGGGCAGC TTTCAATGCC AAATCCACTG 3400
CTGCATGACA GCTCTAGTTT GCCTTTGTGG CTTCTAGCAG 3440
GTGTGGAGCC TGAGCAAAGT TAGGAATTCT GCAGGAAAGA 3480
GGGCAAGGGG CCAGTAAAAG GCAGAGCCAC CTCTATACTG 3520
TAGCAAACAA TTTCTAGATC GTAGAAGCAT AAAACCTTTT 3560
CTGTACAGGT ATTAACTTAC TGGTCTGATT GACAGACTTT 3600
GGTAACAATC CTATGACCCA GAGGGTCTGA GCAGATAGAA 3640
ACCCCAGACA AAGAGTTTGG GGATTAGTTT TGTCATAAGT 3680
GGATTTTTTT GTGAAGTGCA GCAAAGGTTT TTTTTCCTGA 3720
GTGCCTGGTT GTCATTCCTG AA 3922

FIG. 4A

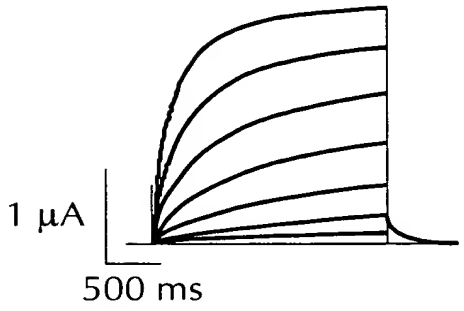

FIG. 4B

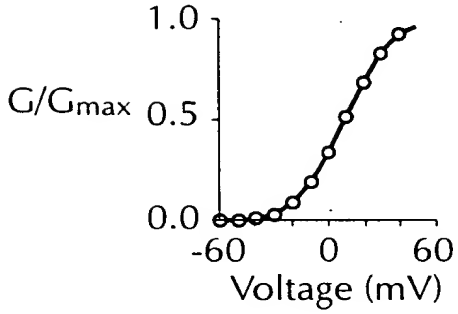

FIG. 4C

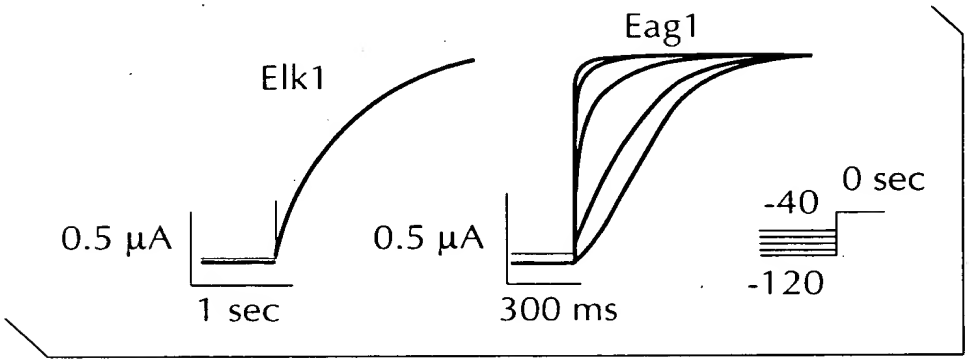

FIG. 4D

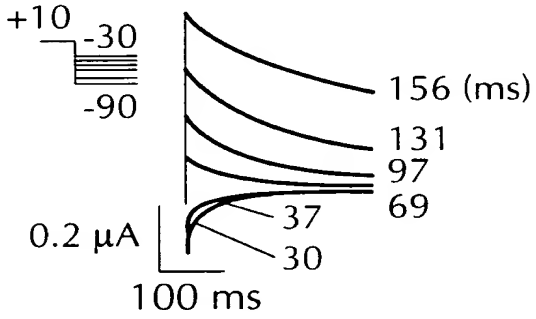

FIG. 4E

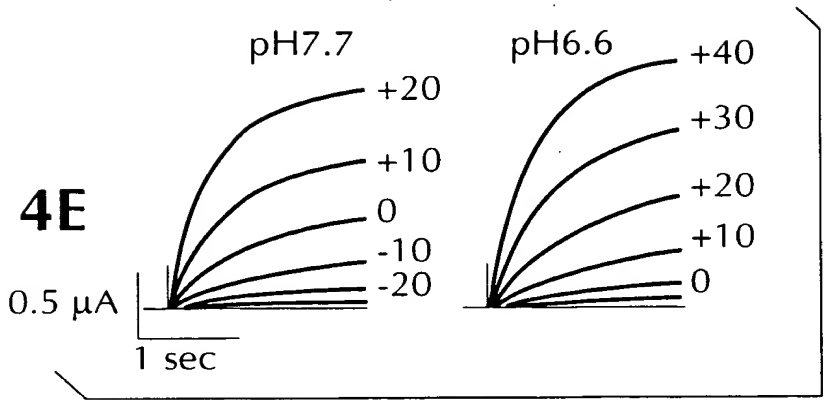

FIG. 4F

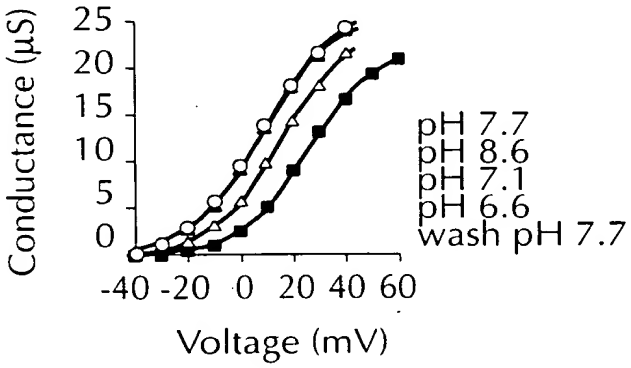

FIG. 4G

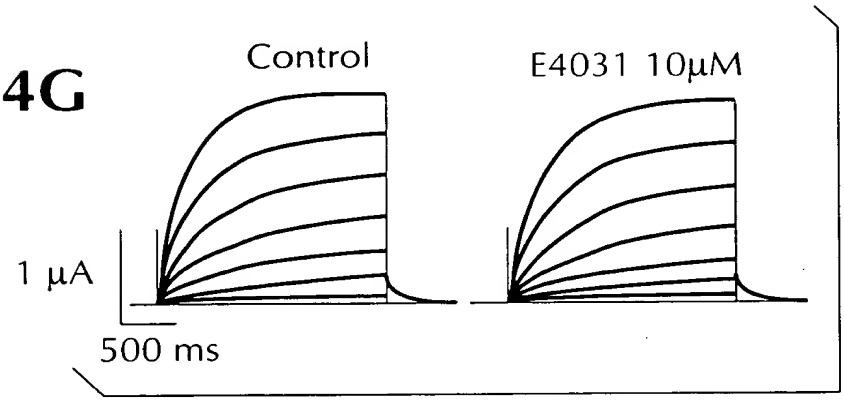

FIG. 4H

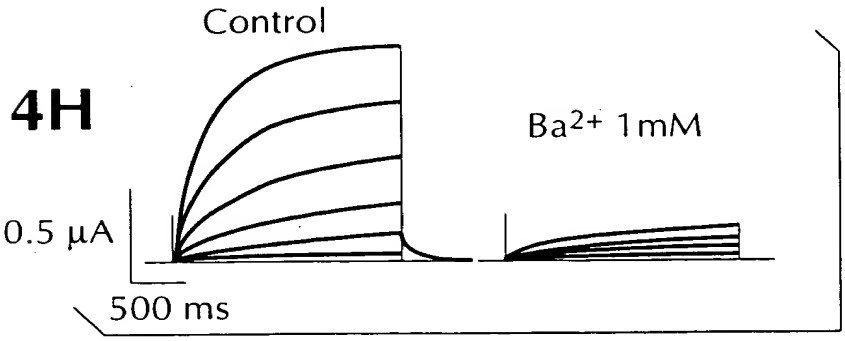

FIG. 5A

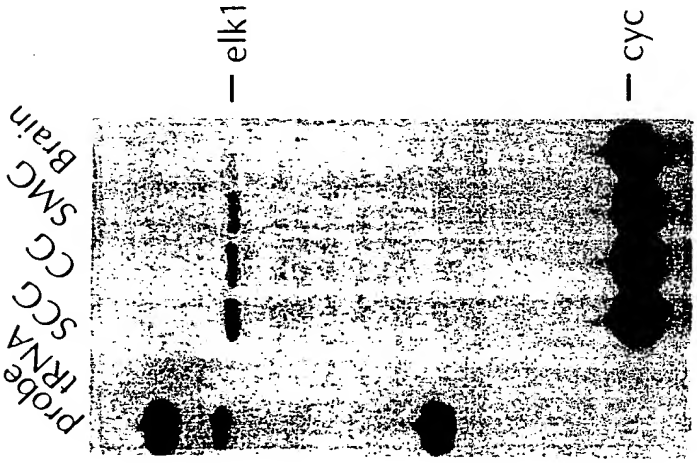

FIG. 5B

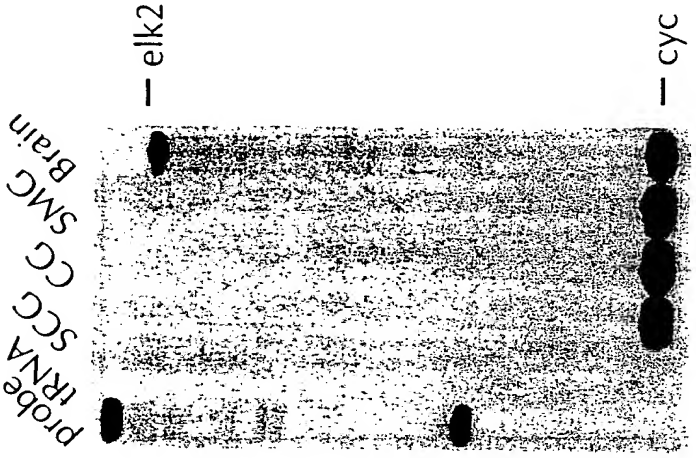

FIG. 5C

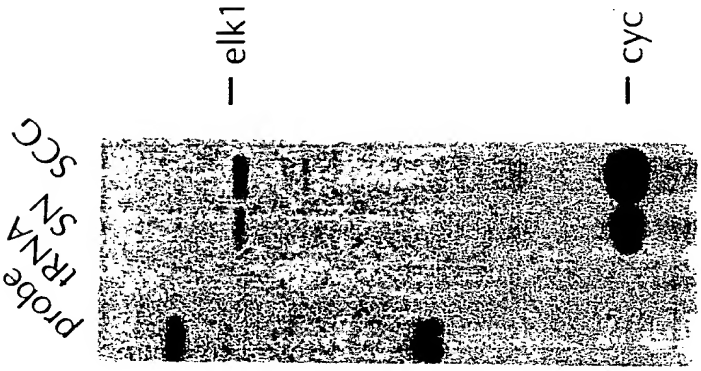

FIG. 5F

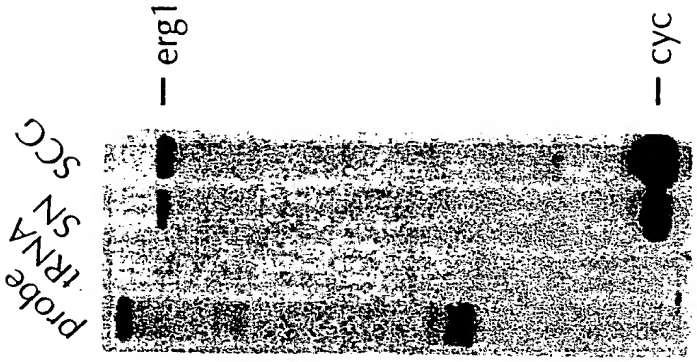

FIG. 5E

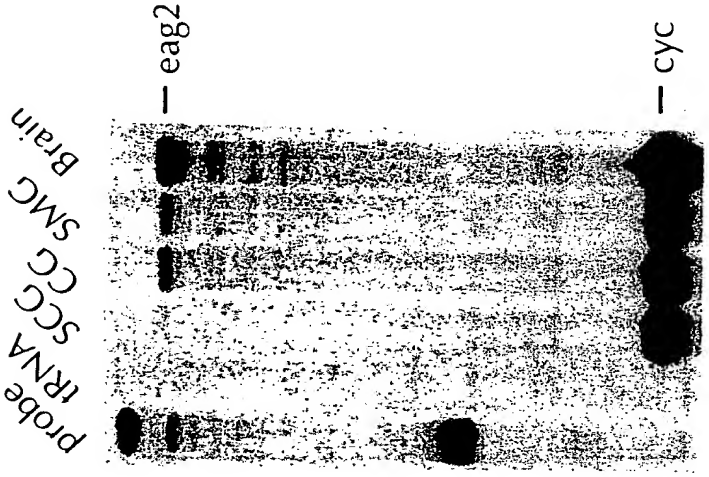
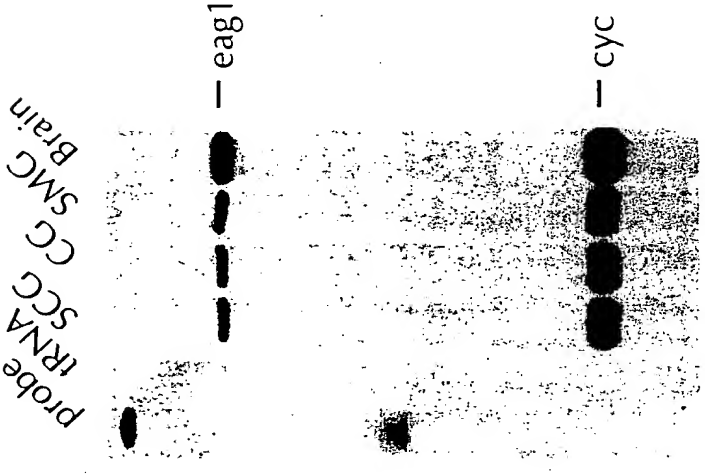
FIG. 5D